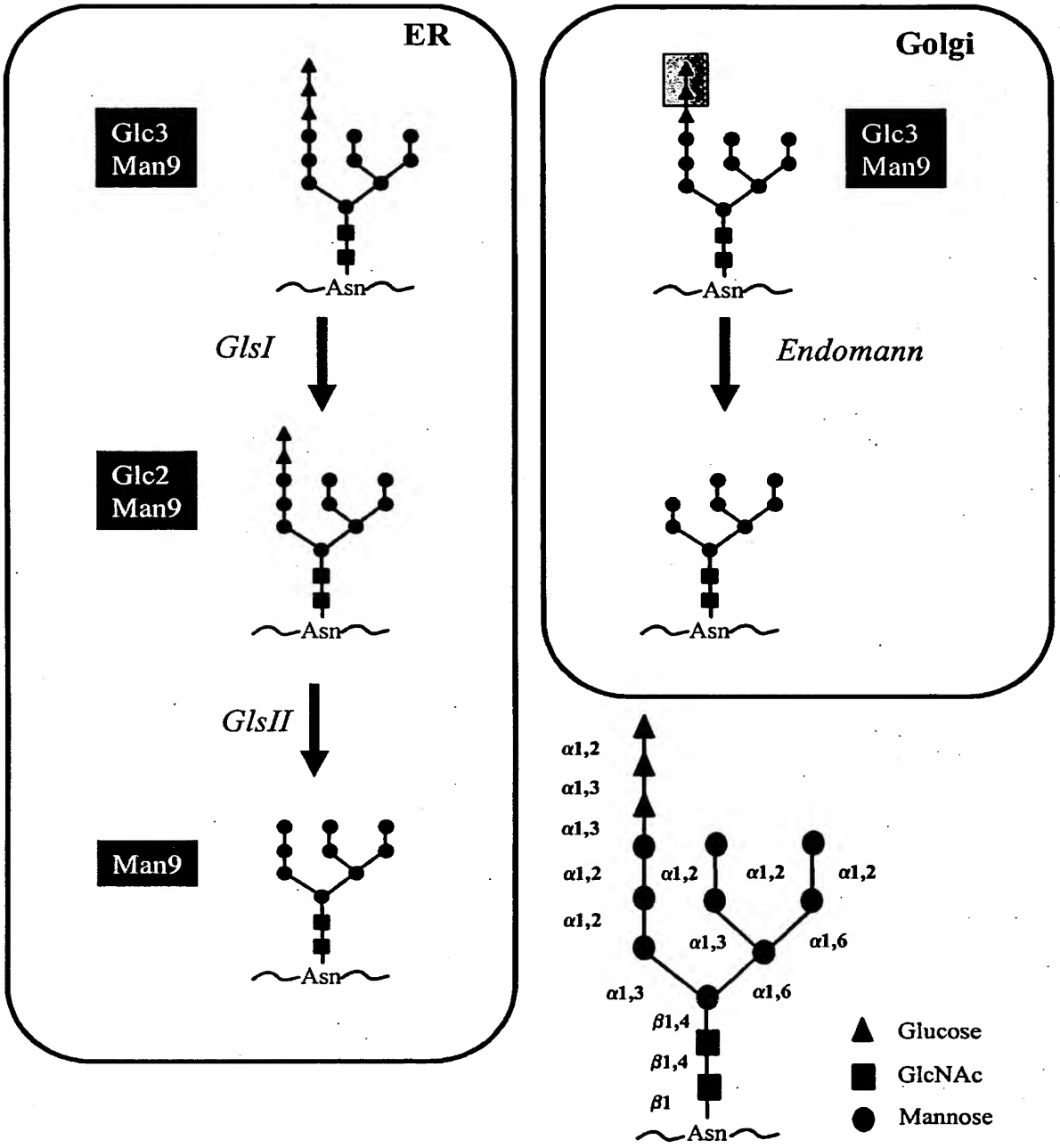
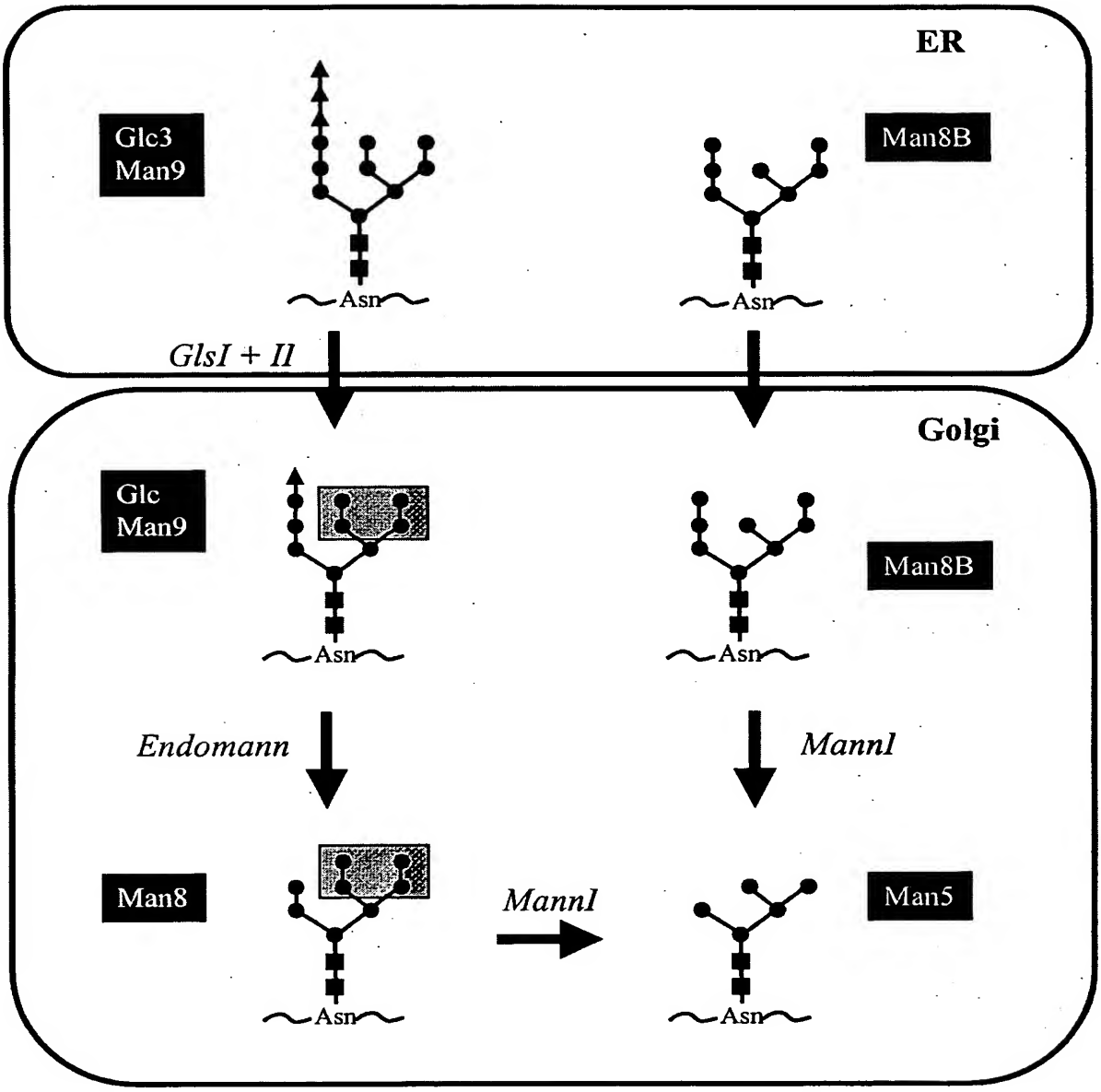


Fig. 1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Man9
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Asn
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Glc
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Asn
Endomann
Mannl
Man8
Mannl
Man5
Asn
Asn

Fig. 2

A

```
>gi|20547442|ref|XP_113472.1|  (XM_113472) hypothetical protein FLJ12838 [Homo sapiens]
          Length = 290

 Score =  526 bits (1354), Expect = e-148
 Identities = 258/290 (88%), Positives = 276/290 (94%)

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           M+QMRSASIGVLALSWYPPD +DENGE TD LVPTILDKAHKYNLKVTFHIEPYSNRDDQ
Sbjct: 1   MRQMRSASIGVLALSWYPPDVNDENGEPTDNLVPTILDKAHKYNLKVTFHIEPYSNRDDQ 60

Query: 222 NMHQNVKYIIDKYGNHPAFYRYKTRMGHSLPMFYIYDSYITKPKTWANLLTPSGSQSVRG 281
           NM++NVKYIIDKYGNHPAFYRYKT+ G++LPMFY+YDSYITKP+ WANLLT SGS+S+R
Sbjct: 61  NMYKNVKYIIDKYGNHPAFYRYKTKTGNALPMFYVYDSYITKPEKWANLLTTSGSRSIRN 120

Query: 282 SPYDGLFIALLVEEKHKYDILQSGFDGIYTYFATNGFTYGSSHQNWNKLKSFCEKNNMIF 341
           SPYDGLFIALLVEEKHKYDILQSGFDGIYTYFATNGFTYGSSHQNW  LK FC+K N+IF
Sbjct: 121 SPYDGLFIALLVEEKHKYDILQSGFDGIYTYFATNGFTYGSSHQNWASLKLFCDKYNLIF 180

Query: 342 IPSVGPGYIDTSIRPWNTQNTRNRINGKYYEVGLSAALQTQPSLISITSFNEWHEGTQIE 401
           IPSVGPGYIDTSIRPWNTQNTRNRINGKYYE+GLSAALQT+PSLISITSFNEWHEGTQIE
Sbjct: 181 IPSVGPGYIDTSIRPWNTQNTRNRINGKYYEIGLSAALQTRPSLISITSFNEWHEGTQIE 240

Query: 402 KAVPKRTANTVYLDYRPHKPSLYLEITRKWSEKYSKERMTYALDQQLPAS 451
           KAVPKRT+NTVYLDYRPHKP LYLE+TRKWSEKYSKER TYALD+QLP S
Sbjct: 241 KAVPKRTSNTVYLDYRPHKPGLYLELTRKWSEKYSKERATYALDRQLPVS 290
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B

```
>gi|18031878|gb|AAL07306.1|  (AY048774) mandaselin short form [Homo sapiens]
          Length = 195

 Score = 49.7 bits (117), Expect = 9e-06
 Identities = 22/23 (95%), Positives = 23/23 (99%)

Query: 1   MRQMRSASIGVLALSWYPPDVND 23
           MRQMRSASIGVLALSWYPPDVN+
Sbjct: 173 MRQMRSASIGVLALSWYPPDVNE 195
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C

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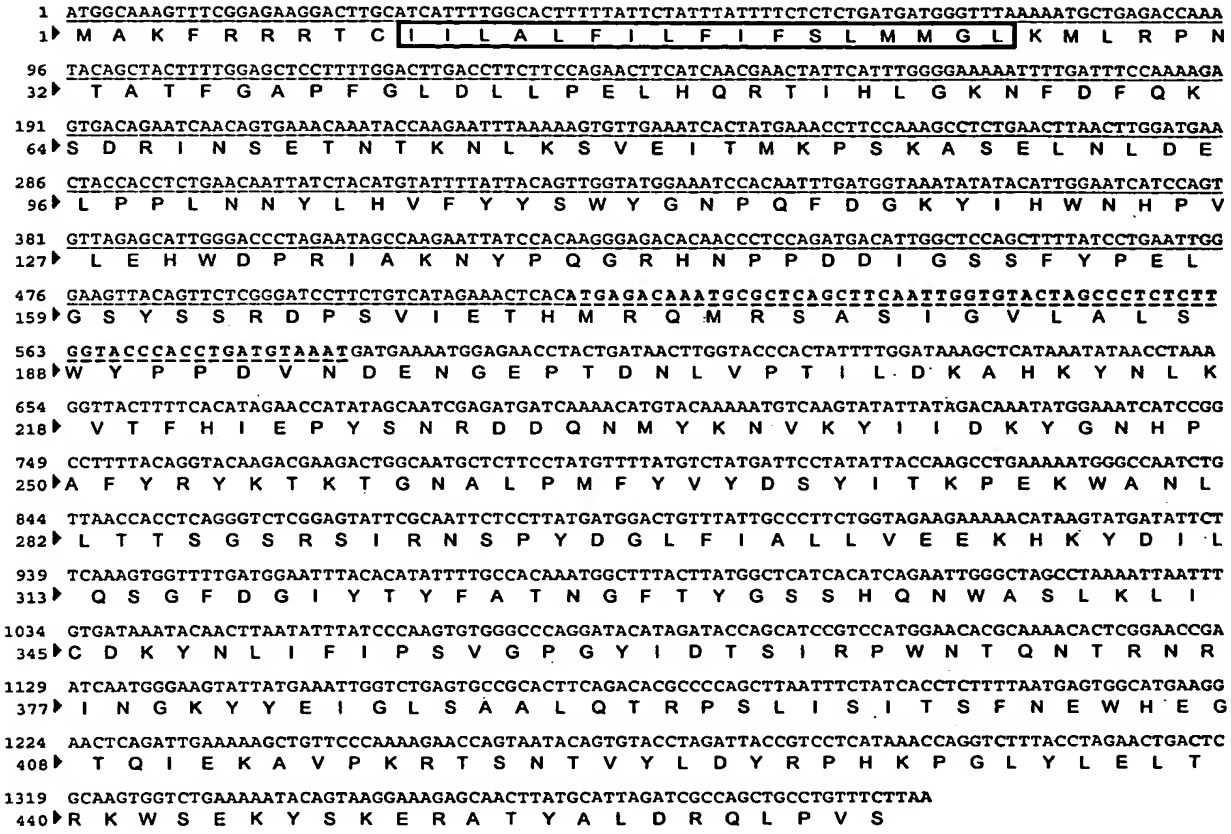
Fig. 3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96 TACAGCTACTTTTGGAGCTCCTTTTGGACTTGACCTTCTTCCAGAACTTCATCAACGAACTATTCATTTGGGGAAAAATTTTGATTTCCAAAAGA
32 T A T F G A P F G L D L L P E L H Q R T I H L G K N F D F Q K
191 GTGACAGAATCAACAGTGAAACAAATACCAAGAATTTAAAAAGTGTTGAAATCACTATGAAACCTTCCAAAGCCTCTGAACTTAACTTGGATGAA
64 S D R I N S E T N T K N L K S V E I T M K P S K A S E L N L D E
286 CTACCACCTCTGAACAATTATCTACATGTATTTTATTACAGTTGGTATGGAAATCCACAATTTGATGGTAAATATATACATTGGAATCATCCAGT
96 L P P L N N Y L H V F Y Y S W Y G N P Q F D G K Y I H W N H P V
381 GTTAGAGCATTGGGACCCTAGAATAGCCAAGAATTATCCACAAGGGAGACACAACCCTCCAGATGACATTGGCTCCAGCTTTTATCCTGAATTGG
127 L E H W D P R I A K N Y P Q G R H N P P D D I G S S F Y P E L
476 GAAGTTACAGTTCTCGGGATCCTTCTGTCATAGAAACTCACATGAGACAAATGCGCTCAGCTTCAATTGGTGTACTAGCCCTCTCTT
159 G S Y S S R D P S V I E T H M R Q M R S A S I G V L A L S
563 GGTACCCACCTGATGTAAATGATGAAAATGGAGAACCTACTGATAACTTGGTACCCACTATTTTGGATAAAGCTCATAAATATAACCTAAA
188 W Y P P D V N D E N G E P T D N L V P T I L D K A H K Y N L K
654 GGTTACTTTTCACATAGAACCATATAGCAATCGAGATGATCAAAACATGTACAAAAATGTCAAGTATATTATAGACAAATATGGAAATCATCCGG
218 V T F H I E P Y S N R D D Q N M Y K N V K Y I I D K Y G N H P
749 CCTTTTACAGGTACAAGACGAAGACTGGCAATGCTCTTCCTATGTTTTATGTCTATGATTCCTATATTACCAAGCCTGAAAAATGGGCCAATCTG
250 A F Y R Y K T K T G N A L P M F Y V Y D S Y I T K P E K W A N L
844 TTAACCACCTCAGGGTCTCGGAGTATTCGCAATTCTCCTTATGATGGACTGTTTATTGCCCTTCTGGTAGAAGAAAAACATAAGTATGATATTCT
282 L T T S G S R S I R N S P Y D G L F I A L L V E E K H K Y D I L
939 TCAAAGTGGTTTTGATGGAATTTACACATATTTTGCCACAAATGGCTTTACTTATGGCTCATCACATCAGAATTGGGCTAGCCTAAAATTAATTT
313 Q S G F D G I Y T Y F A T N G F T Y G S S H Q N W A S L K L I
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345 C D K Y N L I F I P S V G P G Y I D T S I R P W N T Q N T R N R
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377 I N G K Y Y E I G L S A A L Q T R P S L I S I T S F N E W H E G
1224 AACTCAGATTGAAAAAGCTGTTCCCAAAAGAACCAGTAATACAGTGTACCTAGATTACCGTCCTCATAAACCAGGTCTTTACCTAGAACTGACTC
408 T Q I E K A V P K R T S N T V Y L D Y R P H K P G L Y L E L T
1319 GCAAGTGGTCTGAAAAATACAGTAAGGAAAGAGCAACTTATGCATTAGATCGCCAGCTGCCTGTTTCTTAA
440 R K W S E K Y S K E R A T Y A L D R Q L P V S

Fig. 4

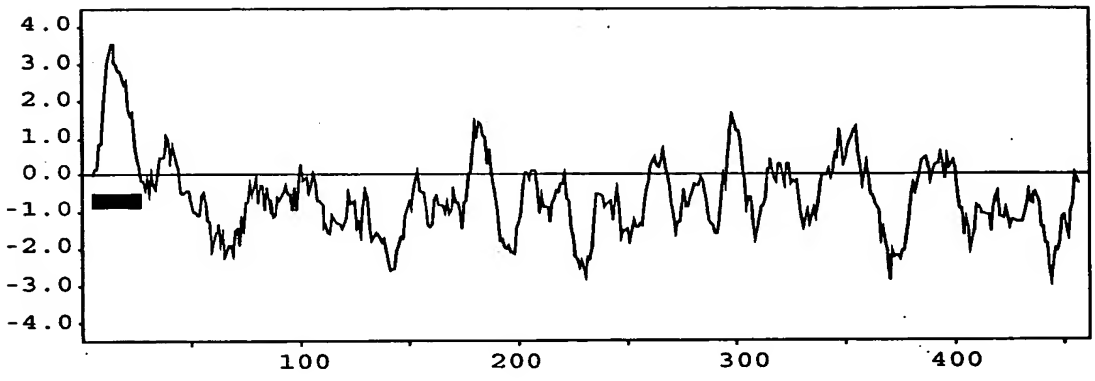

Fig. 5

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  32 N  A  A  S  F  G  P  P  F  G  L  D  L  L  P  E  L  H  P  L  N  A  H  S  G  N  K  A  D  F  Q  R

 189 GAGTGATAGAATCAACATGGAAACAAACACCAAGGCTTTAAAAGGCGCTGGCATGACTGTGCTGCCAGCCAAAGCCTCTGAGGTGAACCTGGAA
  63  S  D  R  I  N  M  E  T  N  T  K  A  L  K  G  A  G  M  T  V  L  P  A  K  A  S  E  V  N  L  E

 283 GAACTACCTCCTCTGAATTACTTTTTACATGCATTTTATTACAGTTGGTATGGAAATCCACAGTTTGATGGTAAATATATACACTGGAATCATC
  95 E  L  P  P  L  N  Y  F  L  H  A  F  Y  Y  S  W  Y  G  N  P  Q  F  D  G  K  Y  I  H  W  N  H

 377 CGGTCCTGGAACACTGGGACCCTCGGATAGCCAAGAACTATCCACAAGGACAACATAGTCCTCCAGACGACATTGGCTCCAGTTTTTATCCTGA
 126 P  V  L  E  H  W  D  P  R  I  A  K  N  Y  P  Q  G  Q  H  S  P  P  D  D  I  G  S  S  F  Y  P  E

 471 GTTAGGAAGTTACAGCTCTCGAGACCCTTCTGTCATAGAAACTCACATGAAACAAATGCGCTCAGCCTCAATTGGAGTTCTGGCCCTGTCTTGG
 157  L  G  S  Y  S  S  R  D  P  S  V  I  E  T  H  M  K  Q  M  R  S  A  S  I  G  V  L  A  L  S  W

 565 TACCCACCTGATTCAAGGGATGACAATGGCGAAGCTACTGATCACTTGGTGCCAACCATTTTGGATAAAGCTCATAAATATAATCTGAAGGTCA
 189 Y  P  P  D  S  R  D  D  N  G  E  A  T  D  H  L  V  P  T  I  L  D  K  A  H  K  Y  N  L  K  V

 659 CTTTTCACATAGAGCCATATAGCAATCGAGATGATCAAAACATGCATCAAAATATCAAGTATATTATAGACAAATATGGAAACCATCCAGCCTT
 220 T  F  H  I  E  P  Y  S  N  R  D  D  Q  N  M  H  Q  N  I  K  Y  I  I  D  K  Y  G  N  H  P  A  F

 753 TTATAGATACAAGACCAGGACTGGGCATTCTCTGCCCATGTTTTATGTCTATGATTCTTACATCACAAAGCCTACAATATGGGCCAATCTGTTA
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1035 TGAAAAGAACAACTTGATGTTTATCCCAAGTGTAGGCCCAGGATACATAGATACAAGCATCCGACCATGGAACACTCAGAACACCCGGAACAGA
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1129 GTCAATGGGAAGTATTATGAAGTTGGTCTAAGTGCTGCACTCCAGACCCACCCCAGTTTAATTTCCATCACCTCTTTCAATGAGTGGCATGAAG
 377 V  N  G  K  Y  Y  E  V  G  L  S  A  A  L  Q  T  H  P  S  L  I  S  I  T  S  F  N  E  W  H  E

1223 GAACTCAAATTGAAAAGGCTGTCCCCAAAAGAACTGCTAACACGATATACCTGGATTACCGGCCTCATAAGCCAAGTCTTTATCTAGAACTAAC
 408 G  T  Q  I  E  K  A  V  P  K  R  T  A  N  T  I  Y  L  D  Y  R  P  H  K  P  S  L  Y  L  E  L  T

1317 TCGAAAGTGGTCTGAAAAATTCAGTAAGGAAAGAATGACGTATGCATTGGATCAACAGCAGCCTGCTTCATAA
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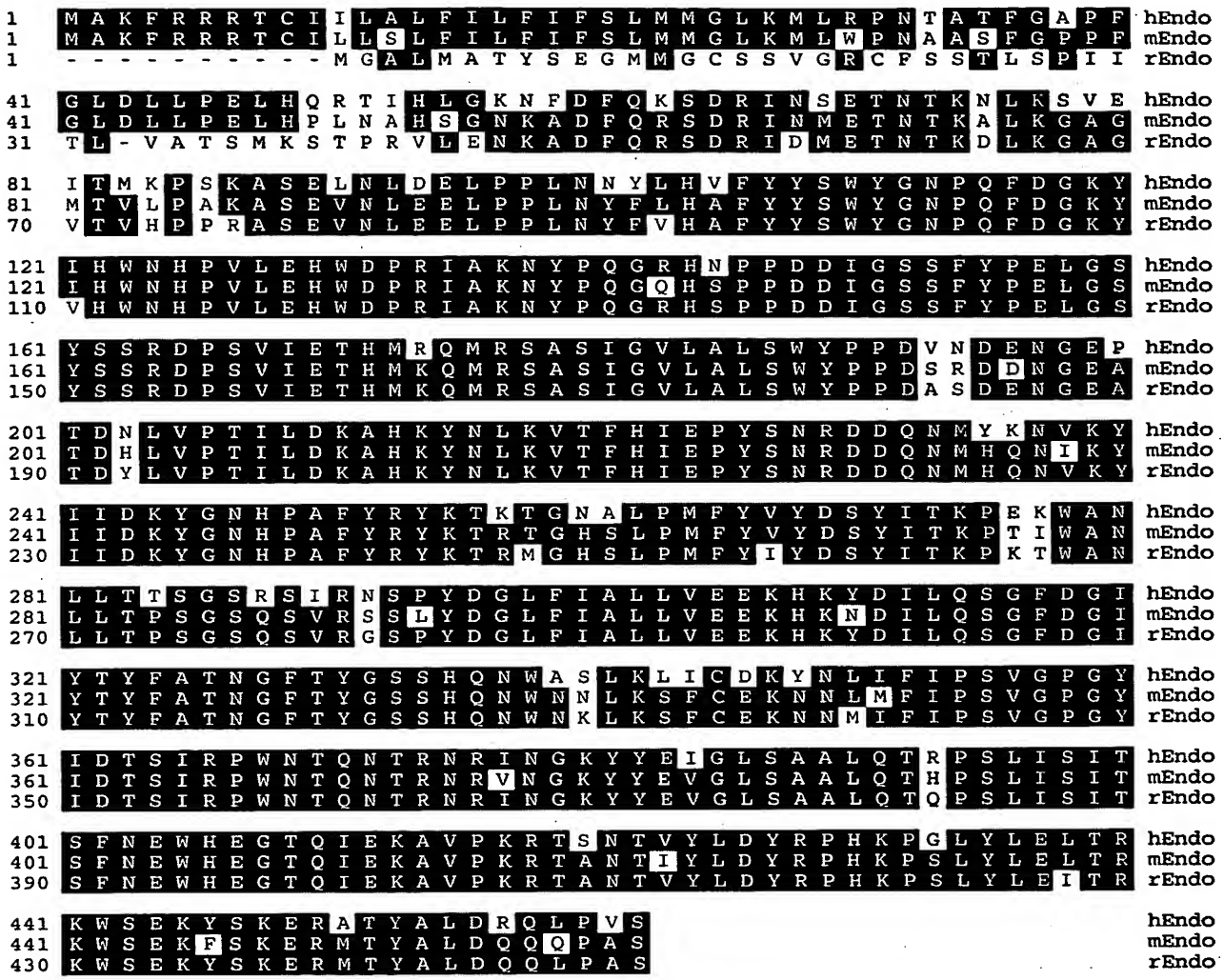
Fig. 6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41 GLDLLPELHPLNAHSGNKADFQRSDRINMETNTKALKGAG mEndo
31 TL-VATSMKSTPRVLENKADFQRSDRIDMETNTKDLKGAG rEndo
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81 MTVLPAKASEVNLEELPPLNYFLHAFYYSWYGNPQFDGKY mEndo
70 VTVHPPRASEVNLEELPPLNYFVHAFYYSWYGNPQFDGKY rEndo
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121 IHWNHPVLEHWDPRIAKNYPQGQHSPPDDIGSSFYPELGS mEndo
110 VHWNHPVLEHWDPRIAKNYPQGRHSPPDDIGSSFYPELGS rEndo
161 YSSRDPSVIETHMRQMRSASIGVLALSWYPPDVNDENGEP hEndo
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150 YSSRDPSVIETHMKQMRSASIGVLALSWYPPDASDENGEA rEndo
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230 IIDKYGNHPAFYRYKTRMGHSLPMFYIYDSYITKPKTWAN rEndo
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281 LLTPSGSQSVRSSLYDGLFIALLVEEKHKNDILQSGFDGI mEndo
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401 SFNEWHEGTQIEKAVPKRTSNTVYLDYRPHKPGLYLELTR hEndo
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390 SFNEWHEGTQIEKAVPKRTANTVYLDYRPHKPSLYLEITR rEndo
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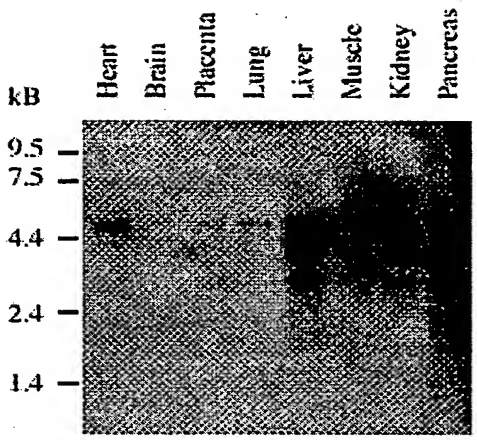
Fig. 7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Brain
Placenta
Lung
Liver
Muscle
Kidney
Pancreas
9.5
7.5
4.4
2.4
1.4

Fig. 8

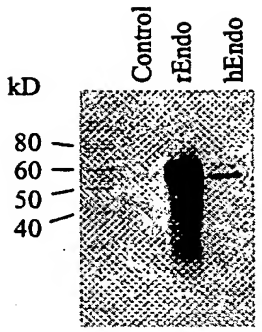


Fig. 9

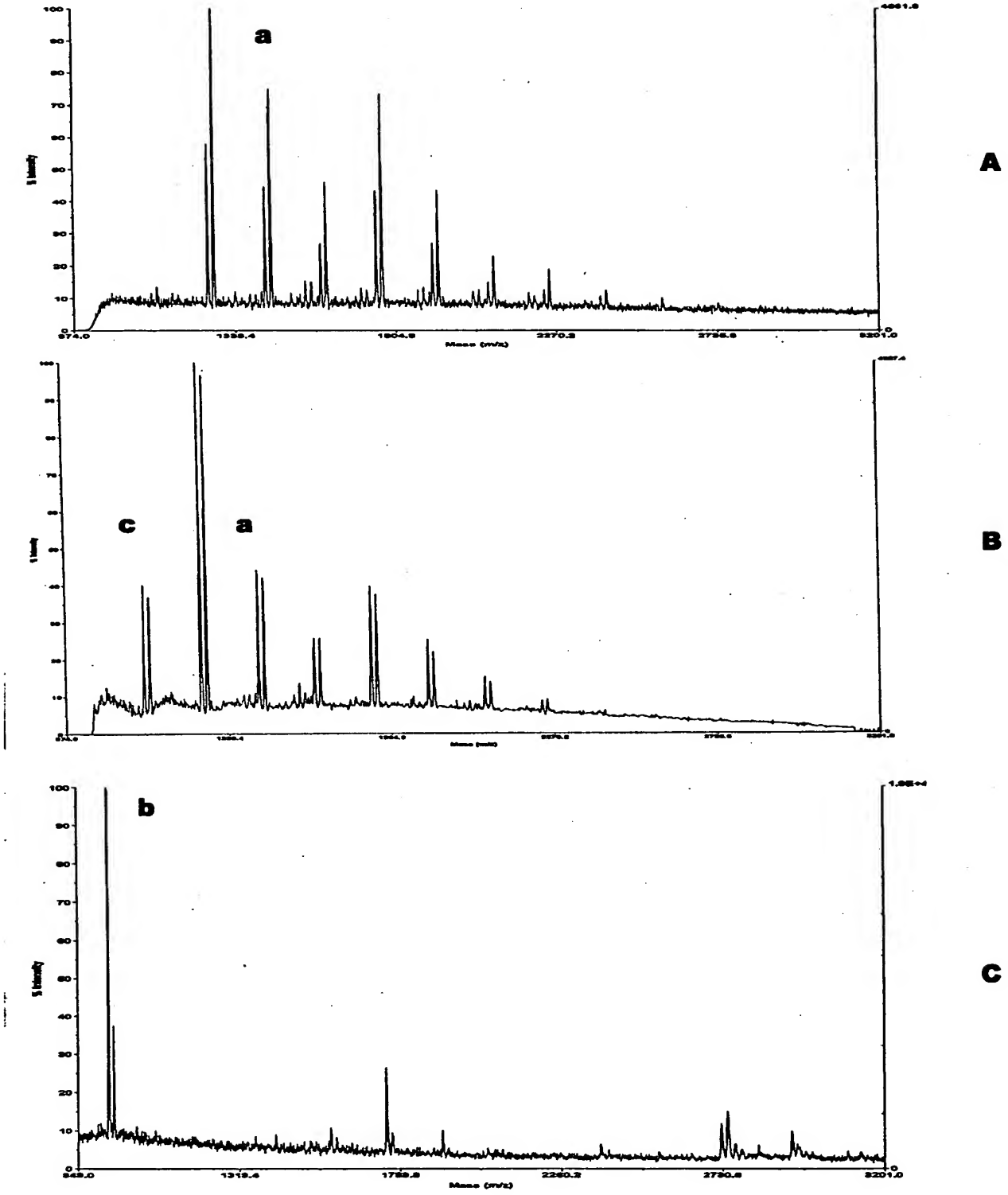


Fig. 10

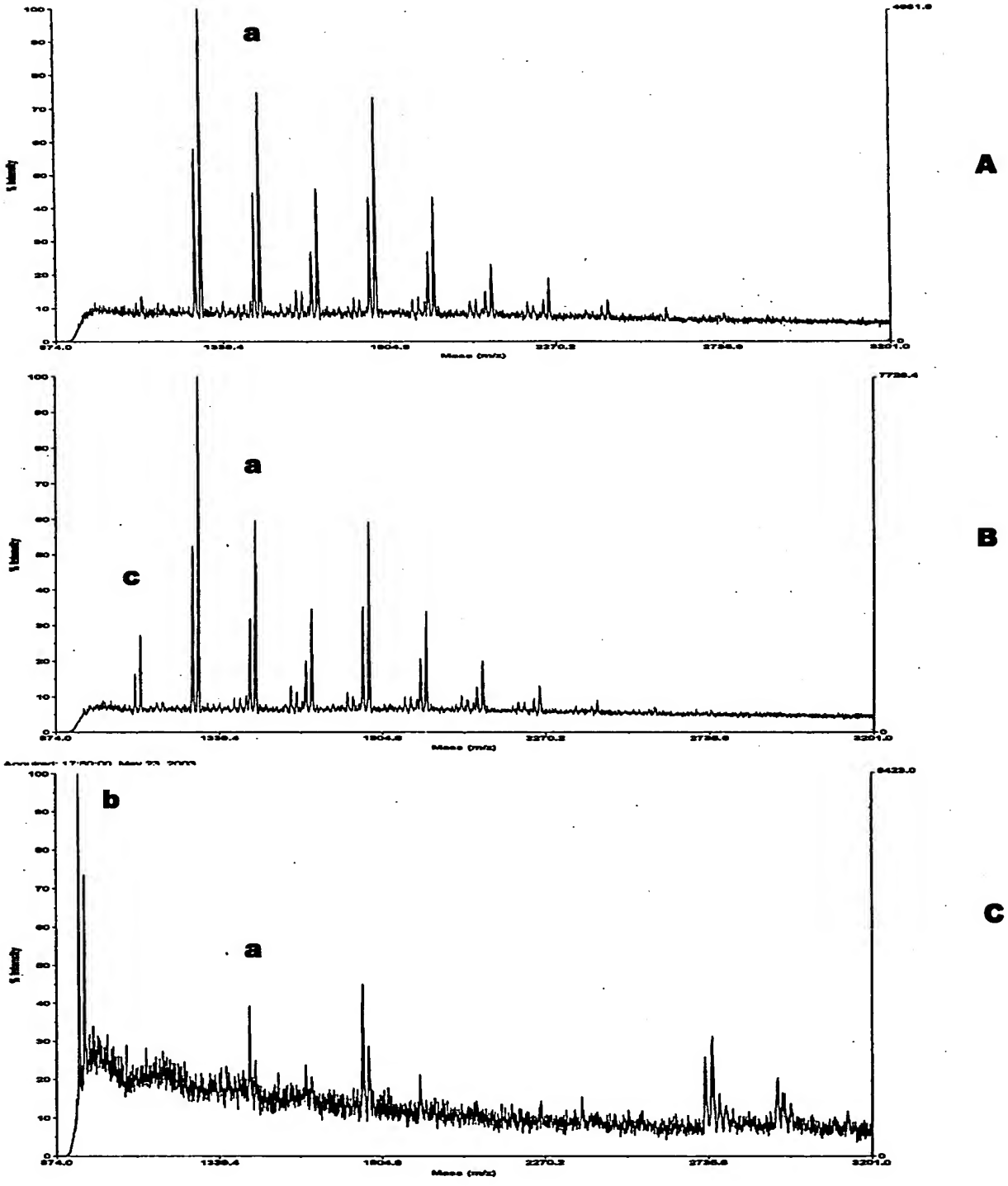


Fig. 11

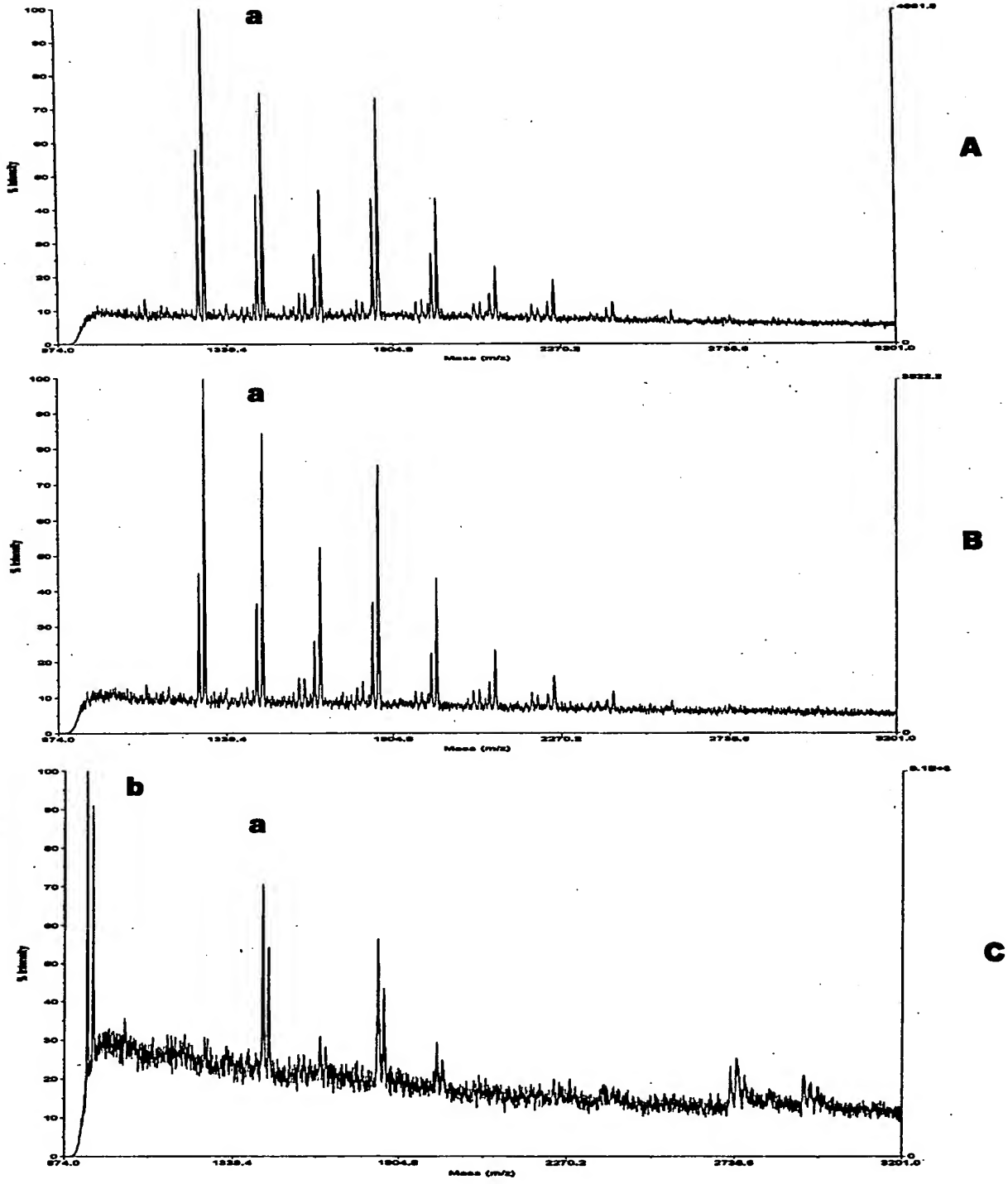
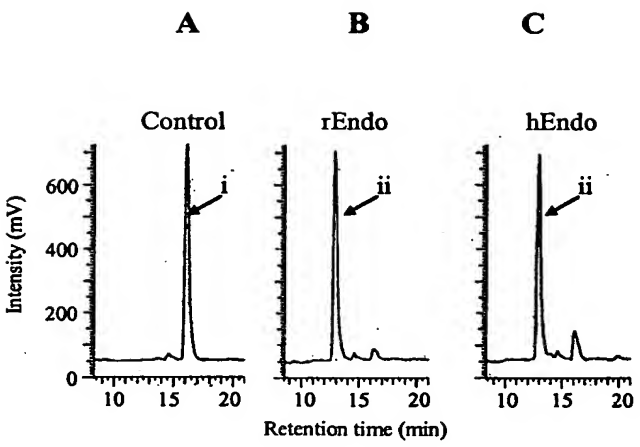


Fig. 12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hEndo
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ii
ii
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400
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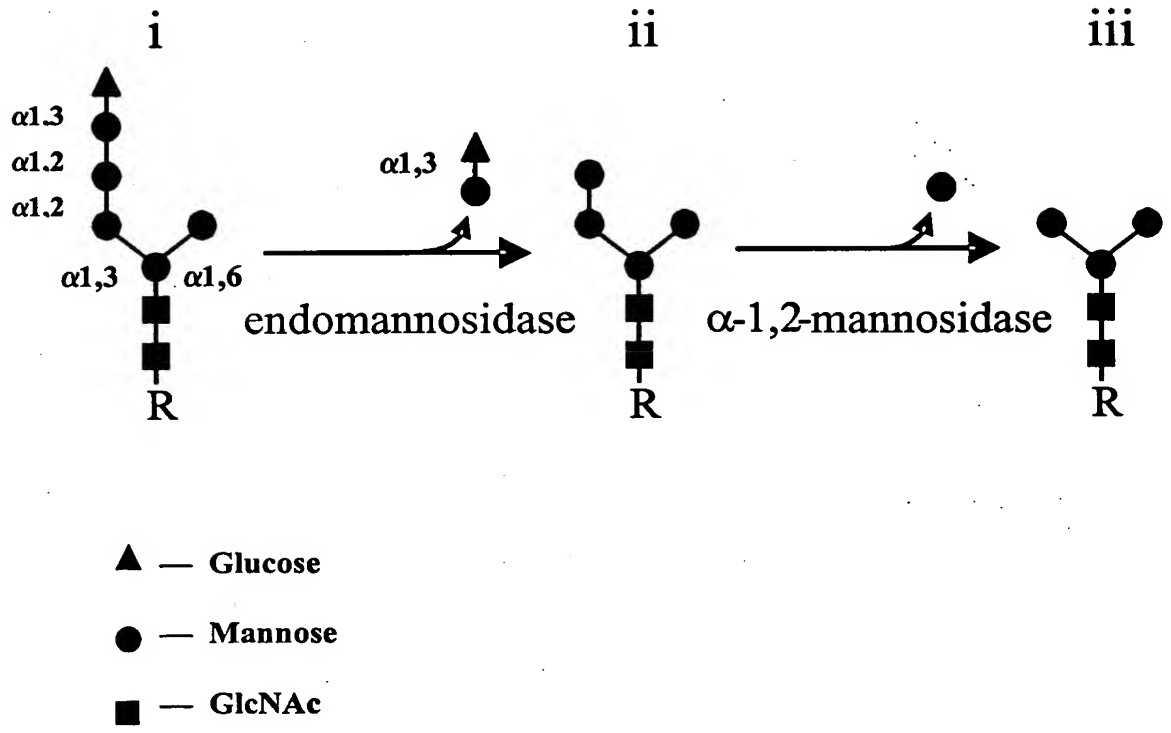
Intensity (mV)
10
15
20
10
15
20
10
15
20
Retention time (min)

Fig. 13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iii
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α1,2
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R
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R
α-1,2-mannosidase
R
▲ — Glucose
● — Mannose
■ — GlcNAc

Fig. 14

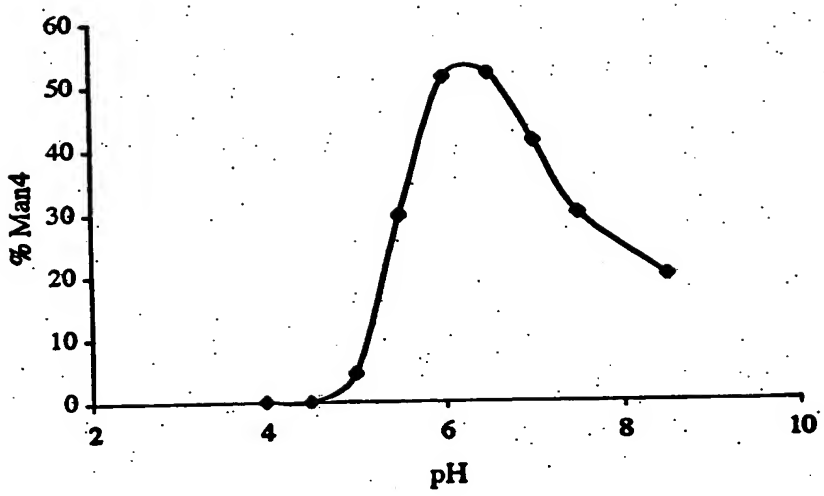

Fig. 15